What is claimed is:

1. Labelled or unlabelled nucleic acid for the specific binding to DNA of human adenoviruses (HAdV DNA), whereby the nucleic acid

a) possesses the sequence SEQ ID NO. 1 or SEQ ID NO. 3,

b) possesses a sequence with a homology greater than 78% with respect to SEQ ID NO. 1 or SEQ ID NO. 3, or

c) is complementary with respect to a nucleic acid according to a) or b).

2. Method for the detection of HAdV DNA in a sample, comprising the following steps:

- Providing a sample possibly containing HAdV DNA,
- Providing a probe that can specifically bind to the DNA of at least 35 different HAdV serotypes,
- Mixing the probe with the sample,
- Amplification of regions of DNA of each of the 35 HAdV serotypes actually present in the sample, so that the section to which said probe can specifically bind is amplified as well,
- Establishing conditions that allow the probe to specifically bind to sections of the amplified regions,
- Detection of the amplified DNA regions to which a probe has bound, quantitatively and/or under real-time conditions.

3. Method for the detection of HAdV DNA in a sample, comprising the following steps:

- Providing a sample possibly containing HAdV DNA,
- Providing at least one primer pair that can specifically bind to the DNA of at least 25 different HAdV serotypes,
- Mixing the at least one primer pair with the sample,
- Establishing conditions that allow one of the primers to specifically bind to one of the DNA strands of every single one of said 25 HAdV types,
- Amplification of the regions – flanked by the at least one primer pair – of the DNA of each of the 25 HAdV serotypes actually present in the sample,

- Detection of amplified DNA regions, quantitatively and/or under real-time conditions.

4. Method for the detection of HAdV DNA in a sample, comprising the following steps:

- Providing a sample possibly containing HAdV DNA,
- Providing at least one primer pair that can specifically bind to the DNA of at least 15 different HAdV serotypes,
- Providing a probe that can specifically bind – in the region flanked by the at least one primer pair – to the DNA of the same at least 15 different HAdV serotypes,
- Mixing the at least one primer pair with the sample,
- Mixing the probe with the sample,
- Establishing conditions that allow one of the primers to anneal to one of the DNA strands of every single one of said 15 HAdV types,
- Amplification of the regions of the DNA - of all of the 15 HAdV serotypes actually present in the sample - flanked by the at least one primer pair,
- Establishing conditions that allow the probe to specifically bind to sections of the amplified regions,
- Detection of amplified DNA regions to which a probe has bound, quantitatively and/or under real-time conditions.

5. Method according to one of claims 2 to 4, characterized in that in the amplification one uses a primer that

a) possesses the sequence SEQ ID NO. 1,
b) possesses a sequence with a homology greater than 78% with respect to SEQ ID NO. 1, or
c) is complementary to a nucleic acid according to a) or b).

6. Method according to claim 5, characterized in that as second primer one uses a primer that

a) possesses the sequence SEQ ID NO. 2,

b) possesses a sequence with a homology greater than 78 % with respect to SEQ ID NO. 2, or

c) is complementary to a nucleic acid according to a) or b).

7. Method according to one of claims 2 and 4 to 6, characterized in that as probe one uses a nucleic acid that

a) possesses the sequence SEQ ID NO. 3,

b) possesses a sequence with homology greater than 78% with respect to SEQ ID NO. 3, or

c) is complementary to a nucleic acid according to a) or b).

8. Method according to one of claims 2 to 7, characterized in that a TaqMan PCR process is used for amplification and detection.

9. Kit, comprising one primer pair, each of which consists of a nucleic acid that

a) possesses the sequence SEQ ID NO. 1 and SEQ ID NO. 2, respectively

b) possesses a sequence with homology of greater than 78% with respect to SEQ ID NO. 1 and SEQ ID NO. 2, respectively, or

c) is complementary to a nucleic acid to a) or b), and

one probe, which

d) possesses the sequence SEQ ID NO. 3,

e) possesses a sequence with homology greater than 78% with respect to SEQ ID NO. 3, or

f) is complementary to a nucleic acid according to d) or e).

10. Use of one or more nucleic acids according to claim 1 or of a kit according to claim 9 in the detection of HAdV DNA.

11. Method to characterize HAdV serotypes, comprising the following steps:

- Detecting HAdV DNA in a sample in accordance with one of claims 2 to 8
- Characterizing detected HAdV DNA that is present in the sample.